

#9

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/774,681

DATE: 09/24/2001

TIME: 11:27:25

Input Set : D:\31333-20001.txt

Output Set: N:\CRF3\09242001\I774681.raw

4 <110> APPLICANT: Sunol Molecular Corporatiopn
5 Sherman, Linda
6 Lustgarten, Joseph
8 <120> TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
9 RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
12 <130> FILE REFERENCE: 31333-20001.01
14 <140> CURRENT APPLICATION NUMBER: US 09/774,681
15 <141> CURRENT FILING DATE: 2001-02-01
17 <150> PRIOR APPLICATION NUMBER: US 08/812,393
18 <151> PRIOR FILING DATE: 1997-03-05
20 <150> PRIOR APPLICATION NUMBER: US 60/012,845
21 <151> PRIOR FILING DATE: 1996-03-05
23 <160> NUMBER OF SEQ ID NOS: 65
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1350
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Polynucleotide derivative of effective T cell
34 receptor
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)...(1350)
39 <400> SEQUENCE: 1

40	ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg	48
41	Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val	
42	1 5 10 15	
44	cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc	96
45	Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser	
46	20 25 30	
48	ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc	144
49	Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser	
50	35 40 45	
52	atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga	192
53	Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg	
54	50 55 60	
56	ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga	240
57	Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg	
58	65 70 75 80	
60	ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att	288
61	Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile	
62	85 90 95	
64	tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
65	Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
66	100 105 110	
68	tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
69	Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	

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70	115	120	125	
72 tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt				432
73 Ser Val Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly				
74 130	135	140		
76 gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca				480
77 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala				
78 145	150	155	160	
80 gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac				528
81 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His				
82 165	170	175		
84 aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg				576
85 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu				
86 180	185	190		
88 atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct				624
89 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro				
90 195	200	205		
92 gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att				672
93 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile				
94 210	215	220		
96 gtg gag ttg ggt acc ccc tct cag aca tca gtg tac ttc tgt gcc agc				720
97 Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser				
98 225	230	235	240	
100 ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag				768
101 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys				
102 245	250	255		
104 ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg				816
105 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val				
106 260	265	270		
108 ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca				864
109 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro				
110 275	280	285		
112 cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca				912
113 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro				
114 290	295	300		
116 tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc				960
117 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu				
118 305	310	315	320	
120 ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc				1008
121 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe				
122 325	330	335		
124 agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc				1056
125 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu				
126 340	345	350		
128 tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac				1104
129 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp				
130 355	360	365		
132 aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag				1152
133 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys				
134 370	375	380		

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```

136 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg      1200
137 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
138 385                      390                      395                      400
140 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag      1248
141 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
142                      405                      410                      415
144 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc      1296
145 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
146                      420                      425                      430
148 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc      1344
149 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg * Ala Ala Ala
150                      435                      440                      445
152 acc gcg      1350
153 Thr Ala
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 449
159 <212> TYPE: PRT
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Deduced amino acid derivative of effective T cell
164      receptor
166 <400> SEQUENCE: 2
167 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
168 1                      5                      10                      15
169 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
170                      20                      25                      30
171 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
172                      35                      40                      45
173 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
174                      50                      55                      60
175 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
176 65                      70                      75                      80
177 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
178                      85                      90                      95
179 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
180                      100                     105                     110
181 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
182                      115                     120                     125
183 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
184                      130                     135                     140
185 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
186 145                      150                     155                     160
187 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
188                      165                     170                     175
189 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
190                      180                     185                     190
191 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
192                      195                     200                     205
193 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile

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```

194      210      215      220
195 Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
196 225      230      235      240
197 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
198      245      250      255
199 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
200      260      265      270
201 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
202      275      280      285
203 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
204      290      295      300
205 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
206 305      310      315      320
207 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
208      325      330      335
209 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
210      340      345      350
211 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
212      355      360      365
213 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
214      370      375      380
215 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
216 385      390      395      400
217 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
218      405      410      415
219 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
220      420      425      430
221 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Ala Ala Thr
222      435      440      445
223 Ala
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 24
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Primer ✓
234 <400> SEQUENCE: 3
235 cccaaggcac tgatgttcat cttc
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 27
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Primer ✓
245 <400> SEQUENCE: 4
246 tgagacaaag tccccaatct ctgacag
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 26
250 <212> TYPE: DNA

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251 <213> ORGANISM: Primer
 253 <220> FEATURE:
 254 <223> OTHER INFORMATION: Primer
 256 <400> SEQUENCE: 5
 257 ctgcagctgc tcctcaagta ctattc 26
 259 <210> SEQ ID NO: 6
 260 <211> LENGTH: 28
 261 <212> TYPE: DNA
 262 <213> ORGANISM: Artificial Sequence
 264 <220> FEATURE:
 265 <223> OTHER INFORMATION: Primer
 267 <400> SEQUENCE: 6
 268 tcccggagaa ggtccacagt tcctcttt 28
 270 <210> SEQ ID NO: 7
 271 <211> LENGTH: 29
 272 <212> TYPE: DNA
 273 <213> ORGANISM: Artificial Sequence
 275 <220> FEATURE:
 276 <223> OTHER INFORMATION: Primer
 278 <400> SEQUENCE: 7
 279 gaagcagcag agggtttgaa gccacatac 29
 281 <210> SEQ ID NO: 8
 282 <211> LENGTH: 27
 283 <212> TYPE: DNA
 284 <213> ORGANISM: Artificial Sequence
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Primer
 289 <400> SEQUENCE: 8
 290 ggcaggtctt cagttgctta tgaaggt 27
 292 <210> SEQ ID NO: 9
 293 <211> LENGTH: 27
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Artificial Sequence
 297 <220> FEATURE:
 298 <223> OTHER INFORMATION: Primer ✓
 300 <400> SEQUENCE: 9
 301 ggttcctctt cagcgtccag aatatgt 27
 303 <210> SEQ ID NO: 10
 304 <211> LENGTH: 27
 305 <212> TYPE: DNA
 306 <213> ORGANISM: Artificial Sequence
 308 <220> FEATURE:
 309 <223> OTHER INFORMATION: Primer ✓
 311 <400> SEQUENCE: 10
 312 gcgaagaact caccctggac tgttcat 27
 314 <210> SEQ ID NO: 11
 315 <211> LENGTH: 30
 316 <212> TYPE: DNA
 317 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/774,681

DATE: 09/24/2001

TIME: 11:27:26

Input Set : D:\31333-20001.txt

Output Set: N:\CRF3\09242001\I774681.raw